

Investigating Dynamic Heat Stress Responses with Diverse Maize Inbreds through Transcriptome Analyses

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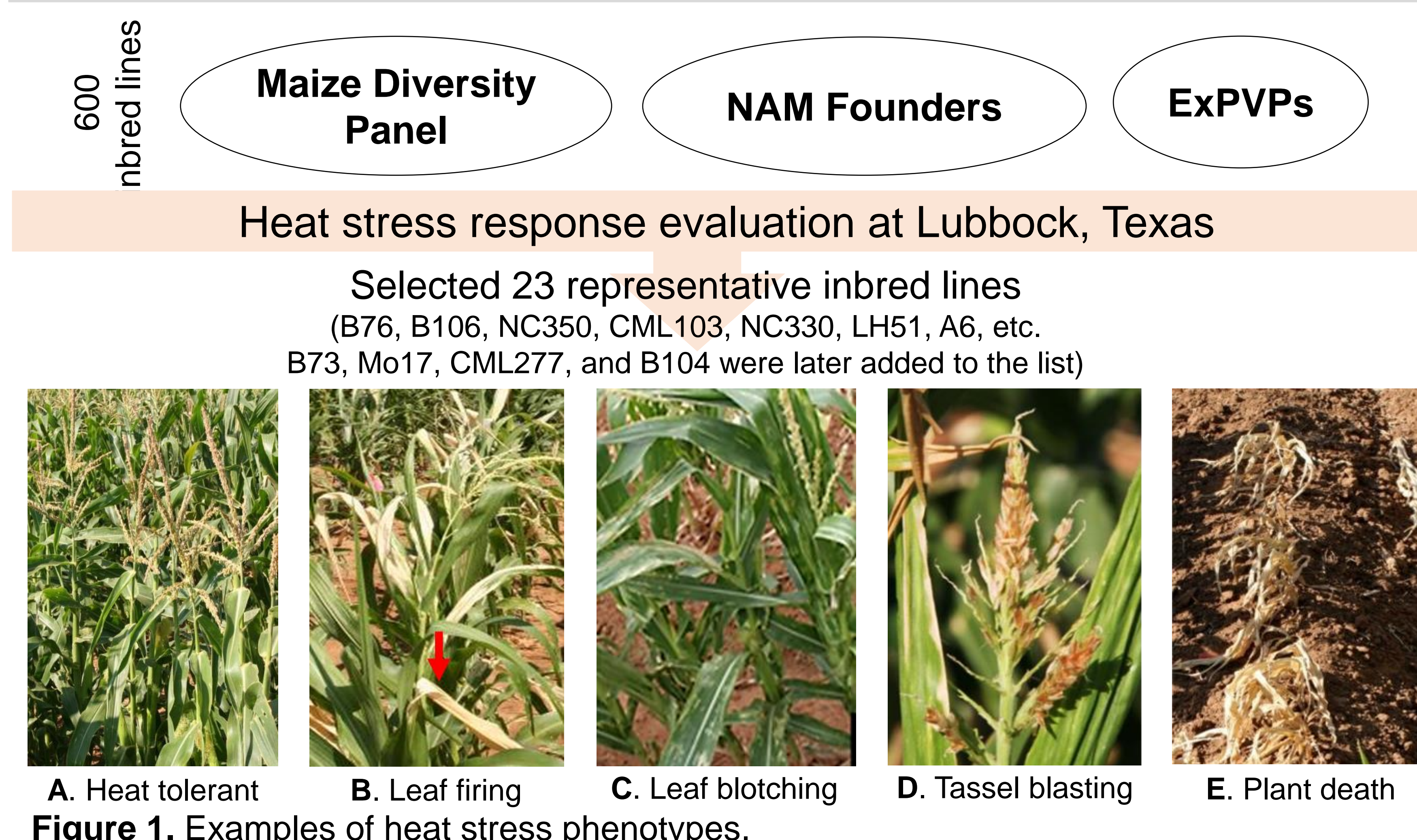
Background

- A better understanding of maize heat stress response mechanisms will facilitate the breeding of heat tolerant varieties.
- Many studies were done focusing on a pair or few contrasting genotypes.

Objectives

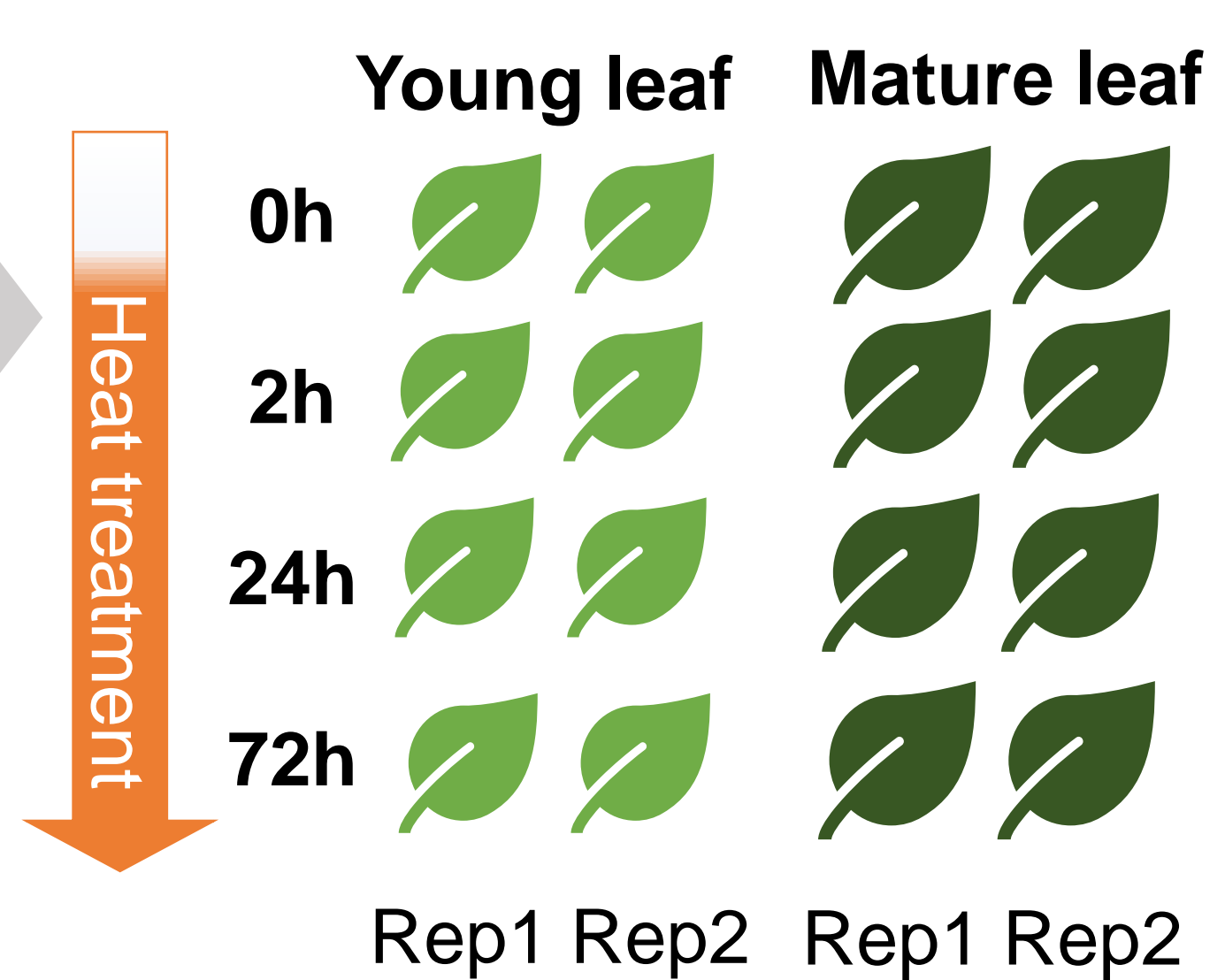
- To quantify the natural variation in heat stress response across diverse maize inbred lines.
- To identify genetic loci contributing to heat stress related phenotypes.
- To identify underlying mechanisms via integrating analyses at the gene expression, biochemical, and whole-plant level.

Materials and Methods



Greenhouse experiment

For each selected inbred line, we collected tissues following:



Data type

- Transcriptome
- Lipidome
- Physiological traits

Workflow

3'mRNA Sequencing
432 samples =
27 genotypes × 4 time points
× 2 leaf types × 2 reps

Define two groups
Tolerant & Sensitive

Differential Expression Analysis Co-expression Network Analysis

Enrichment Analysis
(GO terms, cis-elements, TF families, known TF-target interactions, etc.)

Regulatory Network Inference

Results

Temporal heat response patterns of two groups were uncovered via differential expression analysis.

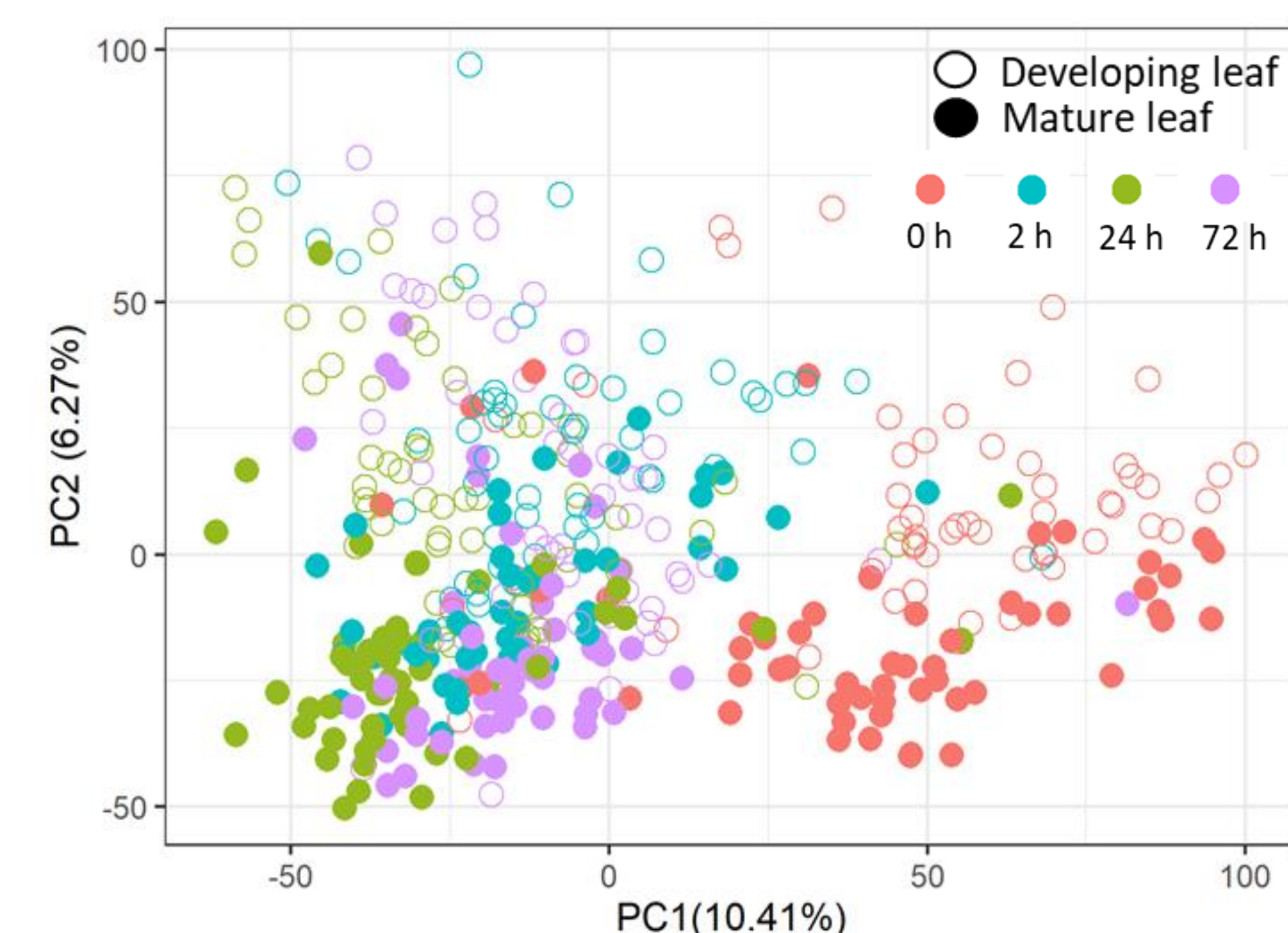


Figure 2. Transcript abundance PCA from 421 samples. Genotypes were classified into T (tolerant) and S (sensitive) groups for downstream analyses.

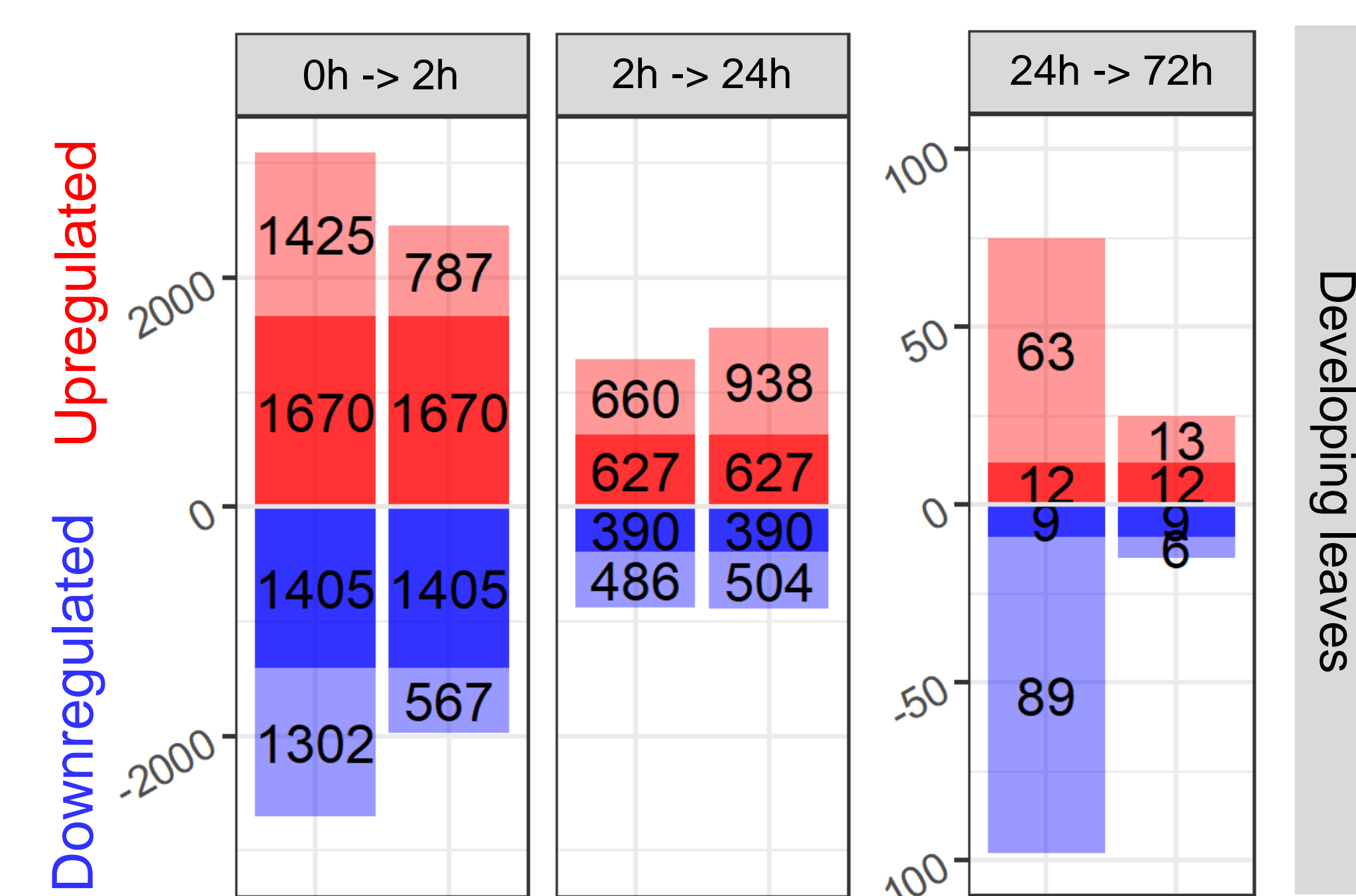


Figure 3. Differentially expressed genes (DEGs) between adjacent time points from T and S groups.

Gene co-expression modules associated with heat tolerance were identified through network analysis.

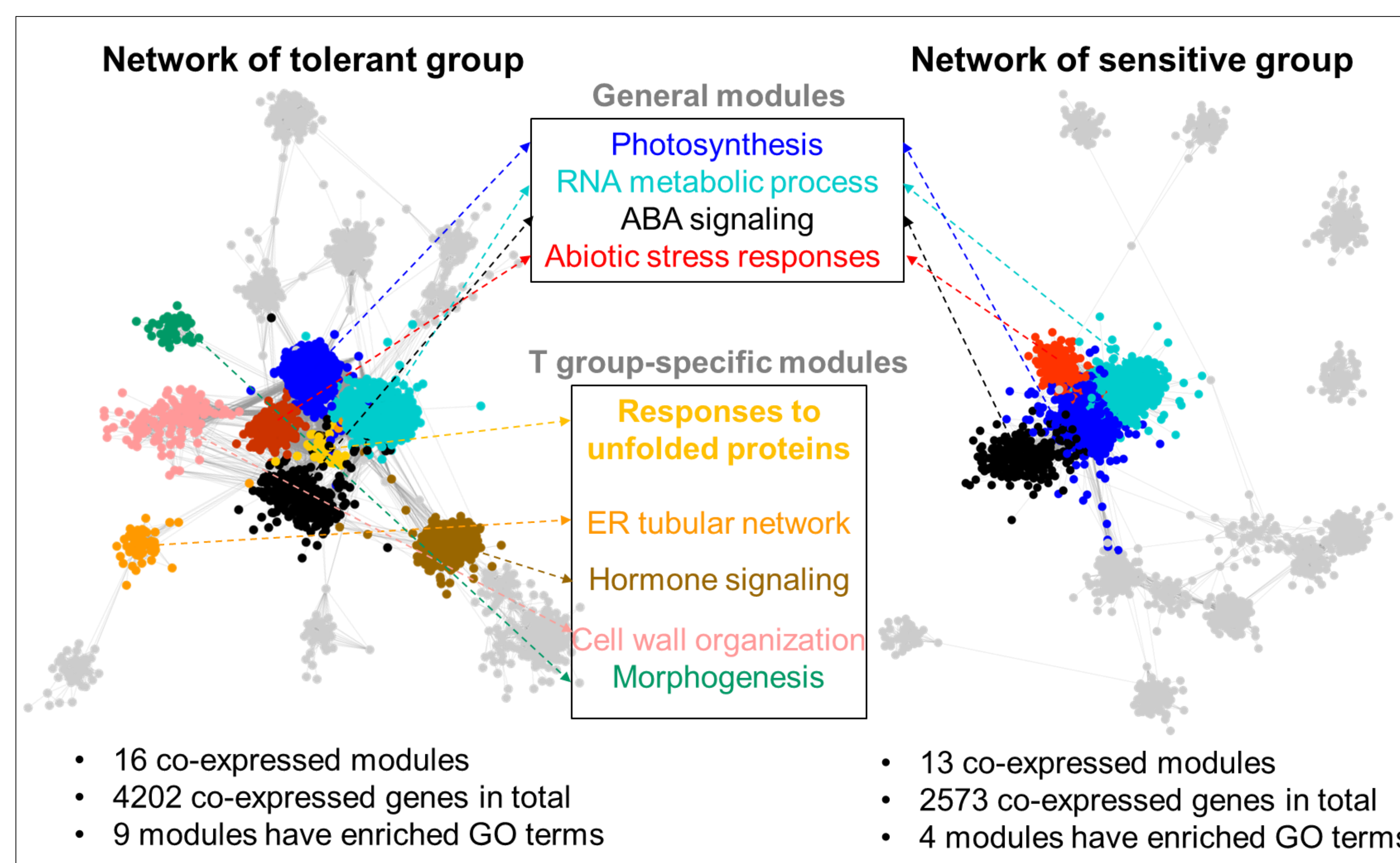


Figure 4. Co-expression networks of two groups under heat stress. The T group-specific yellow module stood out as a key tolerance-related module in the network analysis.

Summary

- Dynamic heat stress response patterns at the transcription level were uncovered through both differential expression and co-expression network analyses.
- Contrasting regulatory networks of the two groups suggested several HSFs as master regulators contributing to the heat tolerance.
- Integrating QTL mappings, lipidome and physiological data will further elucidate the heat stress response mechanisms in maize.

Heat shock factors (HSFs) played a vital role in the regulatory network of the tolerant group.

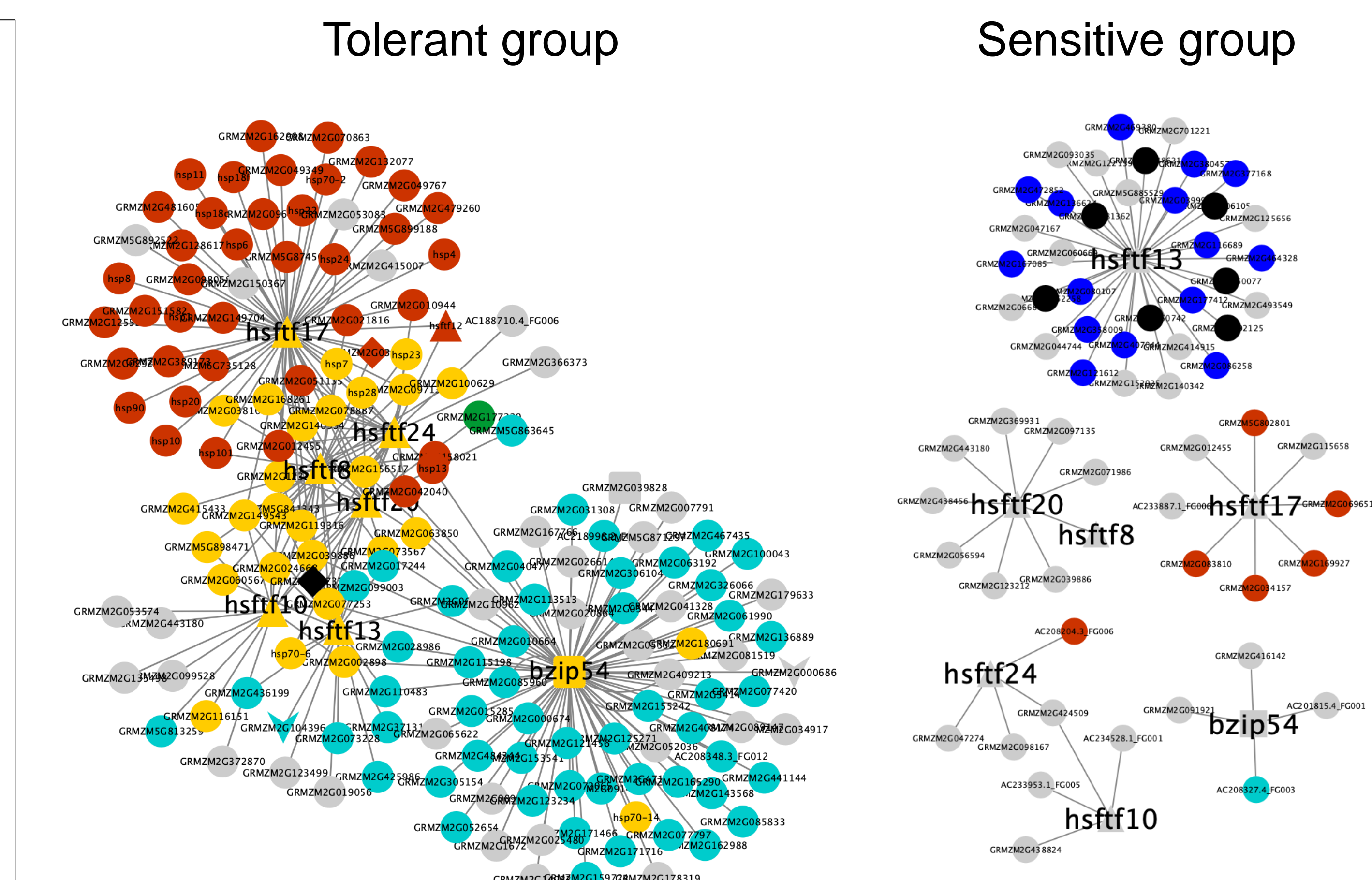


Figure 5. Inferred regulatory networks of selected TFs in the two groups. The putative regulatory relationships of all TFs were obtained using machine learning-based network inference for each group. Results of the 7 TFs (including 6 HSFs) from the T group-specific yellow module were shown here.

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